

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: September 28, 2004, 09:00:23 / Search time 16.2 seconds  
(without alignments)  
57.362 Million cell updates/sec

Title: US-10-084-813-13

Sequence: 1 SOYFPMNFKQIKYVIG 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter 45 summaries

Database: Issued Patents, AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_CONG.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_CONG.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/5A\_CONG.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/5B\_CONG.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/5A\_CONG.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/5B\_CONG.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	54	4 US-08-833-752-11	Sequence 11, Appl
2	96	100.0	352	3 US-08-466-343D-2	Sequence 2, Appl
3	96	100.0	352	3 US-09-087-232A-13	Sequence 13, Appl
4	96	100.0	352	3 US-08-861-105-14	Sequence 14, Appl
5	96	100.0	352	3 US-08-575-967A-2	Sequence 2, Appl
6	96	100.0	352	3 US-09-045-583-52	Sequence 5, Appl
7	96	100.0	352	4 US-09-517-602-5	Sequence 5, Appl
8	96	100.0	352	4 US-09-534-185-52	Sequence 5, Appl
9	96	100.0	352	4 US-08-833-752-5	Sequence 5, Appl
10	96	100.0	352	4 US-09-502-783A-2	Sequence 2, Appl
11	96	100.0	352	4 US-09-796-202-1	Sequence 1, Appl
12	82	85.4	21	3 US-08-907-468-11	Sequence 11, Appl
13	74	77.1	354	4 US-08-724-984A-2	Sequence 13, Appl
14	47	49.0	355	4 US-09-886-319A-13	Sequence 53, Appl
15	45	46.9	355	3 US-09-045-583-53	Sequence 53, Appl
16	45	46.9	355	4 US-09-534-185-53	Sequence 53, Appl
17	43.5	44.3	352	4 US-09-489-039A-13500	Sequence 13500, A
18	43	44.8	172	4 US-09-621-976-4131	Sequence 4131, A
19	43	44.8	344	3 US-08-681-192-2	Sequence 2, Appl
20	42	43.8	460	4 US-08-935-263-4	Sequence 4, Appl
21	42	43.8	460	4 US-09-594-183-4	Sequence 4, Appl
22	42	43.8	160	4 US-09-540-236-3023	Sequence 3023, Ap
23	41	42.7	160	4 US-09-328-352-6593	Sequence 6593, Ap
24	41	42.7	255	4 US-09-491-577-2	Sequence 2, Appl
25	41	42.7	363	4 US-09-252-991A-25052	Sequence 25052, A
26	40	41.7	254	4 US-09-134-001C-4582	Sequence 4582, Ap
27	40	41.7	311	4 US-09-134-001C-5171	Sequence 5171, Ap

28	40	41.7	316	4 US-09-489-039A-8904	Sequence 8904, Ap
29	40	41.7	355	1 US-08-012-988A-2	Sequence 2, Appl
30	40	41.7	355	1 US-08-450-393A-5	Sequence 5, Appl
31	40	41.7	355	3 US-08-446-669-5	Sequence 5, Appl
32	40	41.7	355	4 US-09-239-938-1	Sequence 1, Appl
33	40	41.7	355	4 US-08-833-752-9	Sequence 9, Appl
34	40	41.7	355	4 US-09-886-319A-14	Sequence 14, Appl
35	40	41.7	355	5 PCT-0595-00476-5	Sequence 5, Appl
36	40	41.7	371	3 US-08/622	INFORMATION FOR
37	40	41.7	371	4 US-09-165-923A-10	Sequence 10, Appl
38	40	41.7	659	4 US-08-252-991A-26013	Sequence 26013, A
39	40	41.7	2037	4 US-07-543-681A-3538	Sequence 3538, Ap
40	40	40.6	92	4 US-09-328-352-5171	Sequence 5171, Ap
41	39	40.6	448	4 US-09-134-000C-3794	Sequence 3794, Ap
42	39	40.6	452	4 US-09-530-836-6	Sequence 6, Appl
43	39	40.6	485	4 US-09-134-000C-6031	Sequence 6031, Ap
44	39	40.6	598	2 US-08-853-659A-53	Sequence 53, Appl
45	39	40.6	664	4 US-09-377-497-70	Sequence 70, Appl

## ALIGNMENTS

RESULT 1  
US-08-833-752-11  
Sequence 11, Application US/08833752  
Patent No. 6448375  
GENERAL INFORMATION:  
APPLICANT: SAMSON, MICHEL  
APPLICANT: PARMENTIER, MARC  
APPLICANT: VASSART, GILBERT  
APPLICANT: LIBERT, FREDERICK  
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Krobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,752  
FILING DATE: 9-APR-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 54 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-833-752-11  
Query Match: 100.0%; Score 96; DB 4; Length 54;  
Best Local Similarity: 100.0%; Pred. No. 5e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 9 SOYFPMNFKQIKYVIG 26  
1 SOYFPMNFKQIKYVIG 18  
OY 1 SOYFPMNFKQIKYVIG 18  
DB 9 SOYFPMNFKQIKYVIG 26  
RESULT 2

GenCore version 5.1.6  
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# OM protein - protein search, using nw model

Run on: September 28, 2004, 08:51:21; Search time 52.525 seconds  
(without alignments)  
118.345 Million cell updates/sec

Title: US-10-084-813-12

Sequence: 1 QMDFGNTMCGLTGTYFGTGFPS 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database:

1: Geneseq\_293and4:\*  
2: geneseqp19808:\*  
3: geneseqp19908:\*  
4: geneseqp20008:\*  
5: geneseqp20018:\*  
6: geneseqp20028:\*  
7: geneseqp20038:\*  
8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	126	100.0	22	4 AAB88994	AAB88994 HIV gp120
2	126	100.0	184	2 AAW27406	AAW27406 Inactive
3	126	100.0	215	2 AAW27408	AAW27408 Inactive
4	126	100.0	215	2 AAW88238	AAW88238 HIV-1 co-
5	126	100.0	268	7 ADC10142	ADC10142 Human NOV
6	126	100.0	332	2 AAW26766	AAW26766 Human NOV
7	126	100.0	352	2 AAW27407	AAW27407 Human CCR
8	126	100.0	352	2 AAW27123	AAW27123 Human CCR
9	126	100.0	352	2 AAW27125	AAW27125 Macaque C
10	126	100.0	352	2 AAW27602	AAW27602 Human G-P
11	126	100.0	352	2 AAW27603	AAW27603 Human G-P
12	126	100.0	352	2 AAW27604	AAW27604 Human G-P
13	126	100.0	352	2 AAW27605	AAW27605 Human G-P
14	126	100.0	352	2 AAW27606	AAW27606 Human G-P
15	126	100.0	352	2 AAW27607	AAW27607 Human G-P
16	126	100.0	352	2 AAW27608	AAW27608 Human G-P
17	126	100.0	352	2 AAW27609	AAW27609 Human G-P
18	126	100.0	352	2 AAW27610	AAW27610 Human G-P
19	126	100.0	352	2 AAW27611	AAW27611 Human G-P
20	126	100.0	352	2 AAW27612	AAW27612 Human G-P
21	126	100.0	352	2 AAW27613	AAW27613 Human G-P
22	126	100.0	352	2 AAW27614	AAW27614 Human G-P
23	126	100.0	352	2 AAW27615	AAW27615 Human G-P
24	126	100.0	352	2 AAW27616	AAW27616 Human G-P
25	126	100.0	352	2 AAW27617	AAW27617 Human G-P

26	126	100.0	352	5 AAW27618	AAW27618 Human G-P
27	126	100.0	352	5 AAW27619	AAW27619 Human G-P
28	126	100.0	352	5 AAW27620	AAW27620 Human G-P
29	126	100.0	352	5 AAW27621	AAW27621 Human G-P
30	126	100.0	352	5 AAW27622	AAW27622 Human G-P
31	126	100.0	352	5 AAW27623	AAW27623 Human G-P
32	126	100.0	352	5 AAW27624	AAW27624 Human G-P
33	126	100.0	352	5 AAW27625	AAW27625 Human G-P
34	126	100.0	352	5 AAW27626	AAW27626 Human G-P
35	126	100.0	352	5 AAW27627	AAW27627 Human G-P
36	126	100.0	352	5 AAW27628	AAW27628 Human G-P
37	126	100.0	352	5 AAW27629	AAW27629 Human G-P
38	126	100.0	352	5 AAW27630	AAW27630 Human G-P
39	126	100.0	352	5 AAW27631	AAW27631 Human G-P
40	126	100.0	352	5 AAW27632	AAW27632 Human G-P
41	126	100.0	352	5 AAW27633	AAW27633 Human G-P
42	126	100.0	352	5 AAW27634	AAW27634 Human G-P
43	126	100.0	352	5 AAW27635	AAW27635 Human G-P
44	126	100.0	352	5 AAW27636	AAW27636 Human G-P
45	126	100.0	371	2 AAW27637	AAW27637 Human G-P

## ALIGNMENTS

RESULT 1  
AAB88994 standard, peptide, 22 AA.  
XX AAB88994/  
XX 23-MAY-2001 (first entry)  
XX  
XX HIV gp120 protein binding peptide #87.  
XX  
XX Human chemokine receptor, CD4, HIV, glycoprotein 120, gp120; antagonist;  
XX replication, CCR5, CXCR4, CD4, STRL3.  
XX  
XX Homo sapiens.  
XX  
XX WO200116182-A2.  
XX  
XX 08-MAR-2001.  
XX  
XX 25-MAR-2001, 2000WO-US023505.  
XX  
XX 27-MAR-1999, 99US-0151270P.  
XX  
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Saxinger C;  
XX  
XX WPI: 2001-244398/25.  
XX  
XX Novel polypeptides useful for treating HIV infection, have homology to  
XX regions of domain of human chemokine receptor CCR5, CXCR4 and STRL3,  
XX and binds to HIV gp120 under physiological conditions.  
XX  
XX Claim 21, Page 38, 114pp, English.  
XX  
XX The present invention describes a number of peptides which are able to  
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human  
XX chemokine receptors CCR5, CXCR4 and STRL3, as well as CD4. These are  
XX useful in the treatment of HIV, as they prevent replication of the virus.  
XX The present sequence is an example of a peptide of the invention  
XX  
XX Sequence 22 AA:  
XX  
XX Query Match 100.0%; Score 126; DB 4; Length 22;  
XX Best Local Similarity 100.0%; Pred. No. 1.2e-12;  
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX 1 QMDFGNTMCGLTGTYFGTGFPS 22

DB 1 QMDPGNTMCOILLTGUYPIGFPS 22

## RESULT 2

ID AAM27406 standard; protein, 184 AA.

XX AAM27406;

DT 14-APR-1998 (first entry)

DB Inactive human CCR5.

XX Inactive; human Cys-Cys chemokine receptor-5; CCR5;

XX human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;

XX predisposition; resistance; diagnosis; treatment; prevention;

XX inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;

XX idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;

XX atherosclerosis; autoimmune disorder.

XX Homo sapiens.

XX W09732019-A2.

XX 04-SEP-1997.

XX 28-FEB-1997; 97NC-BE000023.

XX 01-MAR-1996; 96EP-00870021.

XX 06-AUG-1996; 96EP-00870102.

XX (EURO-) EUROSCREEN SA.

XX Samson M, Parmentier M, Vassart G, Libert F;

XX WPI; 1997-479829/44.

XX N-PSDB; AAT90116.

XX Active and inactive forms of human CC chemokine receptor CCR-5 - useful

XX to diagnose, prevent and/or treat inflammatory disorders, autoimmune

XX disease and viral infection.

XX Claim 1; Fig 1a; 94pp; English.

XX The present sequence is an inactive human CC (Cys-Cys) chemokine receptor

XX 5 (CCR5), which is not a receptor of human immunodeficiency virus type 1

XX or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to diagnose, treat

XX and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,

XX glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,

XX viral infections, especially HIV-1 or HIV-2 infection, cancer,

XX atherosclerosis and autoimmune disorders. Subjects that express the

XX inactive receptor have a predisposition, or resistance to HIV-1 and/or

XX HIV-2

XX Sequence 184 AA;

XX Query Match 100.0%; Score 126; DB 2; Length 184;

XX Best Local Similarity 100.0%; Pred. No. 1,2e-11;

XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE Inactive human CCR5.

XX Inactive; human Cys-Cys chemokine receptor 5; CCR5;

XX human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;

XX predisposition; resistance; diagnosis; treatment; prevention;

XX inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;

XX idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;

XX atherosclerosis; autoimmune disorder.

XX Homo sapiens.

XX W09732019-A2.

XX 04-SEP-1997.

XX 28-FEB-1997; 97NC-BE000023.

XX 01-MAR-1996; 96EP-00870021.

XX 06-AUG-1996; 96EP-00870102.

XX (EURO-) EUROSCREEN SA.

XX Samson M, Parmentier M, Vassart G, Libert F;

XX WPI; 1997-479829/44.

XX N-PSDB; AAT90116.

XX Active and inactive forms of human CC chemokine receptor CCR-5 - useful

XX to diagnose, prevent and/or treat inflammatory disorders, autoimmune

XX disease and viral infection.

XX Claim 7; Fig 1d-e; 94pp; English.

XX The present sequence is an inactive human CC (Cys-Cys) chemokine receptor

XX 5 (CCR5), which lacks the last 3 transmembrane regions and the regions

XX involved in G protein-coupling. CCR5 or its cDNA can be used to diagnose,

XX treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,

XX glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,

XX viral infections, especially human immunodeficiency virus type 1 or type

XX 2 (HIV-1 or HIV-2) infection, cancer, atherosclerosis and autoimmune

XX disorders. Subjects that express the inactive receptor have a

XX predisposition, or resistance to HIV-1 and/or HIV-2

XX Sequence 215 AA;

XX Query Match 100.0%; Score 126; DB 2; Length 215;

XX Best Local Similarity 100.0%; Pred. No. 1,5e-11;

XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 QMDPGNTMCOILLTGUYPIGFPS 22

XX 93 QMDPGNTMCOILLTGUYPIGFPS 114

## RESULT 4

ID AAM88238 standard; protein, 215 AA.

XX AAM88238;

XX 15-MAR-1999 (first entry).

DB HIV-1 co-receptor CCR5 variant CCR5-delta32.

XX HIV-1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS;

XX gene therapy; human.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX 32..56

XX /note="transmembrane domain 1"

Tue Sep 28 15:49:55 2004

us-10-084-813-12.ra1

Page 2

US-09-087-232A-17

Sequence 17, Application US/09087232A

Patent No. 6154421

GENERAL INFORMATION:

APPLICANT: Guillemet et al.

TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR

TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSER: Baker & Botts, L.L.P. attn. Lisa Krole

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/087.232A

FILING DATE: 28 MAY 1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/048,057

FILING DATE: 30 MAY 1997

ATTORNEY/AGENT INFORMATION:

NAME: KOLE, LISA B.

REGISTRATION NUMBER: 35,225

REFERENCE/DOCKET NUMBER: AP 31115

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 408-2628

TELEFAX: (212) 765-2519

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-087-232A-17

Query Match

Best Local Similarity 100.0%; Score 126; DB 3; Length 215;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QMDPNTMCOLLTGLTYPIGPPS 22

DB 93 QMDPNTMCOLLTGLTYPIGPPS 114

RESULT 3

US-08-833-752-6

Sequence 6, Application US/0883752

Patent No. 6448375

GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL

APPLICANT: PARENTIER, MARC

APPLICANT: VASSART, GILBERT

APPLICANT: LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINE RECEPTOR

TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSER: Knopbe, Martens, Olson & Bear

STREET: 610 Newport Center Drive 16th floor

CITY: Newport Beach

STATE: CA

COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/833.752

FILING DATE: 9-APR-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-833-752-6

Query Match

Best Local Similarity 100.0%; Score 126; DB 4; Length 215;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QMDPNTMCOLLTGLTYPIGPPS 22

DB 93 QMDPNTMCOLLTGLTYPIGPPS 114

RESULT 4

US-08-466-343D-2

Sequence 2, Application US/08466343D

Patent No. 6025154

GENERAL INFORMATION:

APPLICANT: LI, YI

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN

TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGMR10 (AS AMENDED)

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., NW, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466.343D

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-466-343D-2

Query Match

Best Local Similarity 100.0%; Score 126; DB 3; Length 352;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QMDPNTMCOLLTGLTYPIGPPS 22

DB 93 QMDPNTMCOLLTGLTYPIGPPS 114

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2004, 09:00:23 / Search time 19.8 seconds  
(without alignments)  
57.362 Million cell updates/sec

Title: US-10-084-813-12

Sequence: 126  
1 OMDPNTMCOILYGLYFIFGFS 22

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database:
- 1: /cgm2\_6/prodata/2/1aa/5A\_COMB.pdb.\*
  - 2: /cgm2\_6/prodata/2/1aa/5B\_COMB.pdb.\*
  - 3: /cgm2\_6/prodata/2/1aa/6A\_COMB.pdb.\*
  - 4: /cgm2\_6/prodata/2/1aa/6B\_COMB.pdb.\*
  - 5: /cgm2\_6/prodata/2/1aa/PCITUS\_COMB.pdb.\*
  - 6: /cgm2\_6/prodata/2/1aa/backfill1seq1.pdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	126	100.0	184	4	US-08-833-752-4
2	126	100.0	215	3	US-09-087-232A-17
3	126	100.0	215	4	US-08-833-752-6
4	126	100.0	352	3	US-08-466-343D-2
5	126	100.0	352	3	US-09-087-232A-13
6	126	100.0	352	3	US-08-861-105-14
7	126	100.0	352	3	US-08-575-867A-2
8	126	100.0	352	4	US-09-045-583-52
9	126	100.0	352	4	US-09-517-605-5
10	126	100.0	352	4	US-09-534-185-52
11	126	100.0	352	4	US-08-833-752-5
12	126	100.0	352	4	US-09-502-783A-2
13	126	100.0	352	4	US-09-796-202-1
14	87	69.0	344	3	US-08-466-343D-9
15	87	69.0	347	1	US-08-461-244-3
16	87	69.0	360	1	US-08-450-393A-4
17	87	69.0	360	3	US-08-446-669-4
18	87	69.0	360	3	US-09-045-583-50
19	87	69.0	360	4	US-09-534-185-50
20	87	69.0	360	4	US-08-833-752-7
21	87	69.0	360	4	US-09-131-827A-2
22	87	69.0	360	4	US-09-131-827A-20
23	87	69.0	374	1	US-08-450-393A-2
24	87	69.0	374	1	US-08-450-393A-2
25	87	69.0	374	1	US-08-450-393A-2
26	87	69.0	374	1	US-08-450-393A-2
27	83	63.9	269	1	US-08-307-499-30

28	83	65.9	269	3	US-09-239-268-30	Sequence 30, Appl
29	82	65.1	355	1	US-08-461-244-2	Sequence 2, Appl
30	82	65.1	355	3	US-09-045-583-56	Sequence 56, Appl
31	82	65.1	355	4	US-09-534-185-56	Sequence 56, Appl
32	81	64.3	360	3	US-09-045-583-51	Sequence 51, Appl
33	81	64.3	360	4	US-09-534-185-51	Sequence 51, Appl
34	80	63.5	354	4	US-08-724-984A-2	Sequence 2, Appl
35	76	60.3	355	4	US-09-886-319A-13	Sequence 13, Appl
36	74	58.7	329	4	US-09-502-783A-2	Sequence 2, Appl
37	71	56.3	355	1	US-08-012-988A-2	Sequence 2, Appl
38	71	56.3	355	3	US-08-446-669-5	Sequence 5, Appl
39	71	56.3	355	3	US-09-045-583-53	Sequence 5, Appl
40	71	56.3	355	4	US-09-239-268-1	Sequence 5, Appl
41	71	56.3	355	4	US-09-534-185-53	Sequence 5, Appl
42	71	56.3	355	4	US-09-534-185-53	Sequence 5, Appl
43	71	56.3	355	4	US-09-886-319A-14	Sequence 14, Appl
44	71	56.3	355	5	US-09-886-319A-14	Sequence 5, Appl
45	69	54.8	355	4	US-08-833-752-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1  
US-08-833-752-4  
Sequence 4, Application US/08833752  
Patent No. 6448375  
GENERAL INFORMATION:  
APPLICANT: SAMSON, MICHEL  
APPLICANT: PARENTIER, MARC  
APPLICANT: VASSART, GILBERT  
APPLICANT: LIBERT, FREDERICK  
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Knobb, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,752  
FILING DATE: 9-APR-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel B  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 184 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-833-752-4  
Query Match 100.0% Score 126, DB 4, Length 184;  
Best Local Similarity 100.0% Pred. No. 1.3e-11;  
Matches 22, Conservative 0, Mismatches 0, Indels 0, Gaps 0;  
CY 1 OMDPNTMCOILYGLYFIFGFS 22  
DB 93 OMDPNTMCOILYGLYFIFGFS 114

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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:51:21 / Search time 42.975 Seconds  
(without alignments)  
118.345 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95

Sequence: 1 YAFVGEKRNLYLVFPK 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282347505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_29Jan04:\*  
1: geneseq219808:\*  
2: geneseq219908:\*  
3: geneseq220008:\*  
4: geneseq220108:\*  
5: geneseq220208:\*  
6: geneseq220308:\*  
7: geneseq220408:\*  
8: geneseq220508:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	18	4 AAB88982	AAB88982 HIV gp120
2	95	100.0	18	4 AAB88982	AAB88982 HIV gp120
3	95	100.0	27	5 AAB81475	AAB81475 Human CCR
4	95	100.0	43	5 AAB81475	AAB81475 Human CCR
5	95	100.0	58	5 AAB81475	AAB81475 Human CCR
6	95	100.0	58	5 AAB81475	AAB81475 Human CCR
7	95	100.0	268	7 ADC10144	ADC10144 Human NOV
8	95	100.0	268	7 ADC10144	ADC10144 Human NOV
9	95	100.0	332	2 AAW26766	AAW26766 Human che
10	95	100.0	352	2 AAW27407	AAW27407 Human CCR
11	95	100.0	352	2 AAW27123	AAW27123 Human che
12	95	100.0	352	2 AAW27125	AAW27125 Mecarque c
13	95	100.0	352	2 AAW27602	AAW27602 Human G-P
14	95	100.0	352	2 AAW23835	AAW23835 Human CC
15	95	100.0	352	2 AAW23835	AAW23835 Human CC
16	95	100.0	352	3 AAW23835	AAW23835 Human CC
17	95	100.0	352	3 AAW23835	AAW23835 Human CC
18	95	100.0	352	4 AAW23835	AAW23835 Human CC
19	95	100.0	352	4 AAW23835	AAW23835 Human CC
20	95	100.0	352	4 AAW23835	AAW23835 Human CC
21	95	100.0	352	4 AAW23835	AAW23835 Human CC
22	95	100.0	352	4 AAW23835	AAW23835 Human CC
23	95	100.0	352	4 AAW23835	AAW23835 Human CC
24	95	100.0	352	4 AAW23835	AAW23835 Human CC
25	95	100.0	352	4 AAW23835	AAW23835 Human CC

26	95	100.0	352	4 AAB83354	AAB83354 Human CCR
27	95	100.0	352	4 AAB82948	AAB82948 Human HIV
28	95	100.0	352	4 AAB82948	AAB82948 Human HIV
29	95	100.0	352	4 AAB82948	AAB82948 Human HIV
30	95	100.0	352	4 AAB82948	AAB82948 Human HIV
31	95	100.0	352	4 AAB82948	AAB82948 Human HIV
32	95	100.0	352	4 AAB82948	AAB82948 Human HIV
33	95	100.0	352	4 AAB82948	AAB82948 Human HIV
34	95	100.0	352	4 AAB82948	AAB82948 Human HIV
35	95	100.0	352	4 AAB82948	AAB82948 Human HIV
36	95	100.0	352	4 AAB82948	AAB82948 Human HIV
37	95	100.0	352	4 AAB82948	AAB82948 Human HIV
38	95	100.0	352	4 AAB82948	AAB82948 Human HIV
39	95	100.0	352	4 AAB82948	AAB82948 Human HIV
40	95	100.0	352	4 AAB82948	AAB82948 Human HIV
41	95	100.0	352	4 AAB82948	AAB82948 Human HIV
42	95	100.0	352	4 AAB82948	AAB82948 Human HIV
43	95	100.0	352	4 AAB82948	AAB82948 Human HIV
44	95	100.0	352	4 AAB82948	AAB82948 Human HIV
45	95	100.0	352	4 AAB82948	AAB82948 Human HIV

## ALIGNMENTS

RESULT 1	AAB88982	standard; peptide, 18 AA.
ID	AAB88982	standard; peptide, 18 AA.
AC	AAB88982	
DT	23-MAY-2001	(first entry)
DE	HIV gp120 protein binding peptide #75.	
KN	Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;	
KN	replication; CCR5; CXCR4; CD4; STRL33.	
OS	Homo sapiens.	
PN	WO200116182-A2.	
PD	08-MAR-2001.	
PF	25-ADG-2000; 2000MO-08023505.	
PR	27-ADG-1999; 99US-0151270P.	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
PI	Saxinger C/	
XX	WPI; 2001-244398/25.	
XX	Novel polypeptides useful for treating HIV infection, have homology to	
XX	regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,	
XX	and binds to HIV gp120 under physiological conditions.	
XX	Example 1; Page 37; 114pp; English.	
XX	The present invention describes a number of peptides which are able to	
XX	bind to HIV glycoprotein 120 (gp120). These are similar to the human	
XX	chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are	
XX	useful in the treatment of HIV, as they prevent replication of the virus.	
XX	The present sequence is an example of a peptide of the invention	
XX	Sequence 18 AA;	
XX	Query Match 100.0%; Score 95; DB 4; Length 18;	
XX	Best Local Similarity 100.0%; Pred. No. 8e-09;	
XX	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX	1 YAFVGEKRNLYLVFPK 18	